

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-8 (Canceled).

Claim 9 (Currently Amended): A method of identifying herbicidally active substances, comprising:

- i. bringing a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase encoded by a nucleic acid ~~sequence~~ molecule comprising
 - a) a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1 ~~sequence as claimed in claim 2~~;
 - b) a nucleic acid molecule having a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of SEQ ID NO: 2; or
 - c) [[b]] functional equivalents of the ~~a~~ nucleic acid ~~sequence~~ molecule having a nucleic acid sequence having at least 55% identity with SEQ ID NO:1 ~~with at least 55% identity with SEQ ID NO:1~~; or functional equivalents of the ~~nucleic acid sequence~~ SEQ ID NO:3 ~~with at least 55% identity with SEQ ID NO:3~~; or functional equivalents of the ~~nucleic acid sequence~~ SEQ ID NO: 5 ~~with at least 51% identity with SEQ ID NO:5~~; or
 - d) a nucleic acid molecule having a nucleic acid sequence having at least 69% identity with SEQ ID NO: 1; or
 - e) [[c]] a nucleic acid molecule having a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 ~~with at least 55% identity with SEQ ID NO: 2~~ by back translation; or a ~~nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID~~

~~NO:4 with at least 54% identity with SEQ ID NO: 4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO: 6 by back translation; or~~

f) a nucleic acid molecule having a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO: 2, with at least 73% identity with SEQ ID NO: 2 by back translation;

into contact with one or more test compounds under conditions which permit the test compound(s) to bind to the nucleic acid molecule or to sucrose-6-phosphate phosphatase; and

ii. detecting whether the test compound binds to the sucrose-6-phosphate phosphatase of i); or

iii. detecting whether the test compound reduces or blocks the transcription, translation or expression of the sucrose-6-phosphate phosphatase of i).

Claim 10 (Currently Amended): A method as claimed in claim 9, which comprises

i. either expressing, in a transgenic organism, sucrose-6-phosphate phosphatase encoded by a nucleic acid sequence comprising

a) a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1 sequence as claimed in claim 2;

b) a nucleic acid molecule having a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of SEQ ID NO: 2; or

c) [[b]] ~~functional equivalents of the a nucleic acid sequence molecule having a nucleic acid sequence having at least 55% identity with SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID~~

~~NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO: 5 with at least 51% identity with SEQ ID NO:5; or~~

d) a nucleic acid molecule having a nucleic acid sequence having at least 69% identity with SEQ ID NO: 1; or

e) [[c]] a nucleic acid molecule having a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO: 2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO: 4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO: 6 by back translation; or

f) a nucleic acid molecule having a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO: 2, with at least 73% identity with SEQ ID NO: 2 by back translation; or

culturing an organism which naturally contains sucrose-6-phosphate phosphatase;

ii. bringing the sucrose-6-phosphate phosphatase of step i) in the cell digest of the transgenic or nontransgenic organism, in partially or homogeneously purified form, into contact with a test compound; and

iii. selecting a test compound which reduces or blocks the activity of the sucrose-6-phosphate phosphatase of step a), where the activity of the sucrose-6-phosphate phosphatase incubated with the test compound is compared with the activity of a sucrose-6-phosphate phosphatase which has not been incubated with a test compound.

Claim 11 (Original): A method as claimed in claim 10, wherein, in step iii), the

activity is determined by employing sucrose-6-phosphate as substrate and the orthophosphate which is formed in the reaction is determined quantitatively by means of ammonium molybdate.

Claim 12 (Currently Amended): A method as claimed in claim 9, further comprising

i. generating a nonhuman transgenic organism selected from the group consisting of bacteria, yeasts, fungi, animal cells and plant cells, as claimed in claim 7 or a transgenic organism comprising a nucleic acid sequence encoding a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase comprising

a) a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1;

b) a nucleic acid molecule having a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of SEQ ID NO: 2; or

[[b]]c) functional equivalents of the a nucleic acid sequence molecule having a nucleic acid sequence having at least 55% identity with SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5; or

d) a nucleic acid molecule having a nucleic acid sequence having at least 69% identity with SEQ ID NO: 1; or

[[c]]e) a nucleic acid molecule having a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity

~~with SEQ ID NO:6 by back translation; where the polypeptide with the biological activity of a sucrose-6 phosphate phosphatase is overexpressed in the transgenic organism; and or~~

f) a nucleic acid molecule having a nucleic acid sequence, which on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO: 2, with at least 73% identity with SEQ ID NO: 2, by back translation; and

ii. applying a test substance to the transgenic organism of i) and to a nontransgenic organism of the same genotype; and

iii. determining the growth or the viability of the transgenic and the nontransgenic organisms after application of the test substance; and

iv. thereby selecting test substances which bring about reduced growth or reduced viability of the nontransgenic organism in comparison with the growth of the transgenic organism.

Claim 13 (Original): A method as claimed in claim 12, which is carried out in a plant organism, a cyanobacterium or a proteobacterium.

Claim 14 (Canceled).

Claim 15 (Previously presented): A method as claimed in claim 9, 10 or 11, wherein the substances are identified in a high-throughput screening.

Claims 16-25 (Canceled).

Claim 26 (New): The method of claim 12, wherein the nucleic acid sequence encoding the polypeptide sequence is in an expression cassette comprising genetic control sequences in operable linkage with the nucleic acid sequence.

Claim 27 (New): The method of claim 26, wherein the expression cassette is contained in a vector.